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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/875,076

DATE: 11/30/2001

TIME: 15:59:59

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Output Set : N:\CRF3\11212001\I875076.raw

3 <110> APPLICANT: Chen, Ruoping
4 Dang, Huong T.
5 Liaw, Chen W.
6 Lin, I-Lin
8 <120> TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
10 <130> FILE REFERENCE: AREN0050
12 <140> CURRENT APPLICATION NUMBER: 09/875,076
13 <141> CURRENT FILING DATE: 2001-06-06
15 <150> PRIOR APPLICATION NUMBER: 09/417,044
16 <151> PRIOR FILING DATE: 1999-10-12
18 <150> PRIOR APPLICATION NUMBER: 60/120,416
19 <151> PRIOR FILING DATE: 1999-02-16
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22 <151> PRIOR FILING DATE: 1999-02-26
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25 <151> PRIOR FILING DATE: 1999-03-12
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64 <151> PRIOR FILING DATE: 1999-10-01
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90 agtccattgc ttagatatag ttttgaaacc atggctccca ctggtttgag ttccttgacc 180
91 gtgaatagta cagctgtgcc cacaacacca gcagcattta agagccctaaa ctgacctctt 240
92 cagatcaccc tttctgctat aatgatattc attctgtttg tgtcttttct tgggaaattg 300
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94 gccagcctag cttttgcaga catgttgctt gcagtgtga acatgccctt tgccctggta 420
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123 Pro Pro Phe Gln His Pro Asp Leu Ser Pro Leu Leu Arg Tyr Ser Phe
124 35 40 45
126 Glu Thr Met Ala Pro Thr Gly Leu Ser Ser Leu Thr Val Asn Ser Thr
127 50 55 60
129 Ala Val Pro Thr Thr Pro Ala Ala Phe Lys Ser Leu Asn Leu Pro Leu
130 65 70 75 80
132 Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu Phe Val Ser Phe
133 85 90 95
135 Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln Lys Ala Ala Met

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142          130          135          140
144 Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val Ser Ala Met Phe
145 145          150          155          160
147 Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu Leu Ile Ile Ser
148          165          170          175
150 Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp Lys Leu Asn Pro
151          180          185          190
153 Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala Thr Ser Phe Cys
154          195          200          205
156 Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu Gln Ile Pro Ser
157          210          215          220
159 Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn Pro Gly Tyr Gln
160 225          230          235          240
162 Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe Ile Pro Phe Leu
163          245          250          255
165 Val Ile Leu Tyr Ser Phe Met Gly Ile Leu Asn Thr Leu Arg His Asn
166          260          265          270
168 Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala
169          275          280          285
171 Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile
172          290          295          300
174 Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe
175 305          310          315          320
177 Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val
178          325          330          335
180 Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile
181          340          345          350
183 Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro
184          355          360          365
186 Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp
187          370          375          380
189 Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr
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207 gcgctagccc tctgggtctt cctgcgcgcg ctgcgcgtgc actcggtggt gaggctgtac 180
208 atgtgtaacc tggcgccag cgacctgtc ttcacctct cgctgccgt tegtctctcc 240

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211 gccgcccacg tgcacccgct gcgactgcgc cacctggcgc ggccccgcgt gccgcgctg 420
212 ctctgcctgg gctgtgtggg gctcatcctg gtgtttgcgc tgcccgcgc ccgcgtgcac 480
213 aggcctctgc gttgccgcta ccgggacctc gaggtgcgc tatgcttga gagcttcagc 540
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215 ctgctgcccc tggcgcggt ggtctactcg tcgggcgcg tcttctggac gctggcgcg 660
216 ccgcagccca cgcagagcca gcggcgcgcg aagaccgtgc gctctctgt ggctaacctc 720
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231 <400> SEQUENCE: 4

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236 20 25 30
238 Leu Ala Ala Gly Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu
239 35 40 45
241 Arg Ala Leu Arg Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu
242 50 55 60
244 Ala Ala Ser Asp Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser
245 65 70 75 80
247 Tyr Tyr Ala Leu His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr
248 85 90 95
250 Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu
251 100 105 110
253 Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg
254 115 120 125
256 Leu Arg His Leu Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly
257 130 135 140
259 Val Trp Ala Leu Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His
260 145 150 155 160
262 Arg Pro Ser Arg Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe
263 165 170 175
265 Glu Ser Phe Ser Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val
266 180 185 190
268 Leu Leu Ala Glu Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val
269 195 200 205
271 Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr
272 210 215 220
274 Gln Ser Gln Arg Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu

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Output Set: N:\CRF3\11212001\I875076.raw

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275 225                230                235                240
277 Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val
278                245                250                255
280 Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg
281                260                265                270
283 Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala
284                275                280                285
286 Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe
287                290                295                300
289 Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser
290 305                310                315                320
292 Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala
293                325                330                335
295 Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu
296                340                345                350
298 Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln
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326 ctggggcgcc tctctcgcc tgcactgcct ggacctgtgc gggcctgcac tccgcaagcc 960
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